```
cons.aa          G G  G V                A K          E
hTGFBR-II  LDTLVGKGRFAEVYKAKLKQNTSEQFETVAVKIFPYDHYASWKDRKDIFSDINLKHENILQF
mActR-IIB  LLEIKARGRFGCVWKAQLMN------DFVAVKIKPLQDKQSWQSEREIFSTPGMKHENLLQF
mActR-II   LLEVKARGRFGCVWKAQLLN------EYVAVKIFPIQDKQSWQNEYEVYSIPGMKHENILQF
daf-1      LFGRVGSGRFGNVSRGDYRG------EAVAVKVFNAIDEPAFHKEIEIFETRMLRHPNVLRY
subdomains       I                        II        III          IV

hTGFBR-II  LTAEERKTELGKQYWLITAFHAKGNLQEYLTRHVISWEDLRNVGSSLARGLSHLHSDHTP-C
mActR-IIB  IAAEKRGSNLEVELWLITAFHDKGSLIDYLKGNIITWNELCHVAETMSRGISYLHEDVPWCR
mActR-II   IGAEKRGTSVDVDLWLITAFHEKGSLSDFLKANVVSWNELCHIAETMARGLAYLHEDIPGLK
daf-1      IGSDRVDTGFVTELWLVIEYHPSGSLHDFLLENTVNIETYYNLMRSTASGLAFLHNQIGGSK
subdomains                          V                        VI-A

cons.aa            DLK  N          DFG
hTGFBR-II  -GRPKMPIVHRDLKSSNILVKNDLTCCLCDFGLSLRL---GPYSSVDDLANSGQVGTARYMAP
mActR-IIB  GEGHKPSIAHRDFKSKNVLLKSDLTAVLADFGLAVRF---EPGKPPGD--THGQVGTRRYMAP
mActR-II   -DGHKPAISHRDIKSKNVLLKNNLTACIADFGLALKF---EAGKSAGD--THGQVGTRRYMAP
daf-1      -ESNKPAMAHRDIKSKNIMYKNDLTCAIGDLGLSLSKPEDAASDIIAN--ENYKCGTVRYLAP
subdomains      VI-B                      VII                    VIII
```

Fig. 1

a.a C C E G N M C

5′ GCGGATCCTGTTGTGAAGGNAATATGTG 3′ Fig. 2A

BAMHI C C G C

a.a V A V K I F

5′ GCGGATCCGTCGCAGTCAAAATTTT 3′ Fig. 2B

BamHI G C G G C

T T T A

a.a R D I K S K N

5′ GCGGATCCGCGATATTAAAAGCAA 3′ Fig. 2C

BAMHI A C C GTCT

G A

a.a E P A M Y

5′ CGGAATTCTGGTGCCATATA Fig. 2D

EcoRI G G G

A A

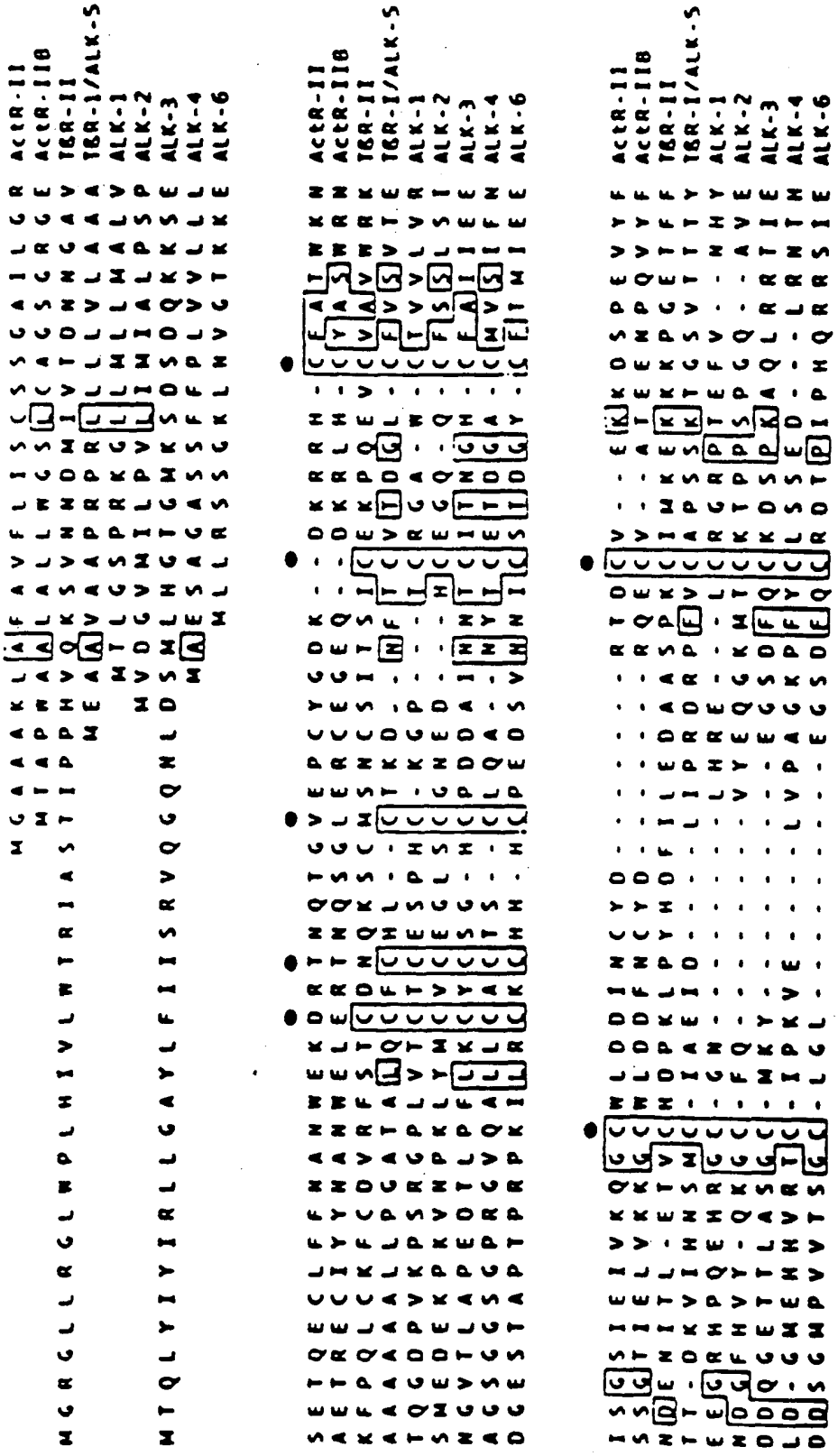

Fig.3

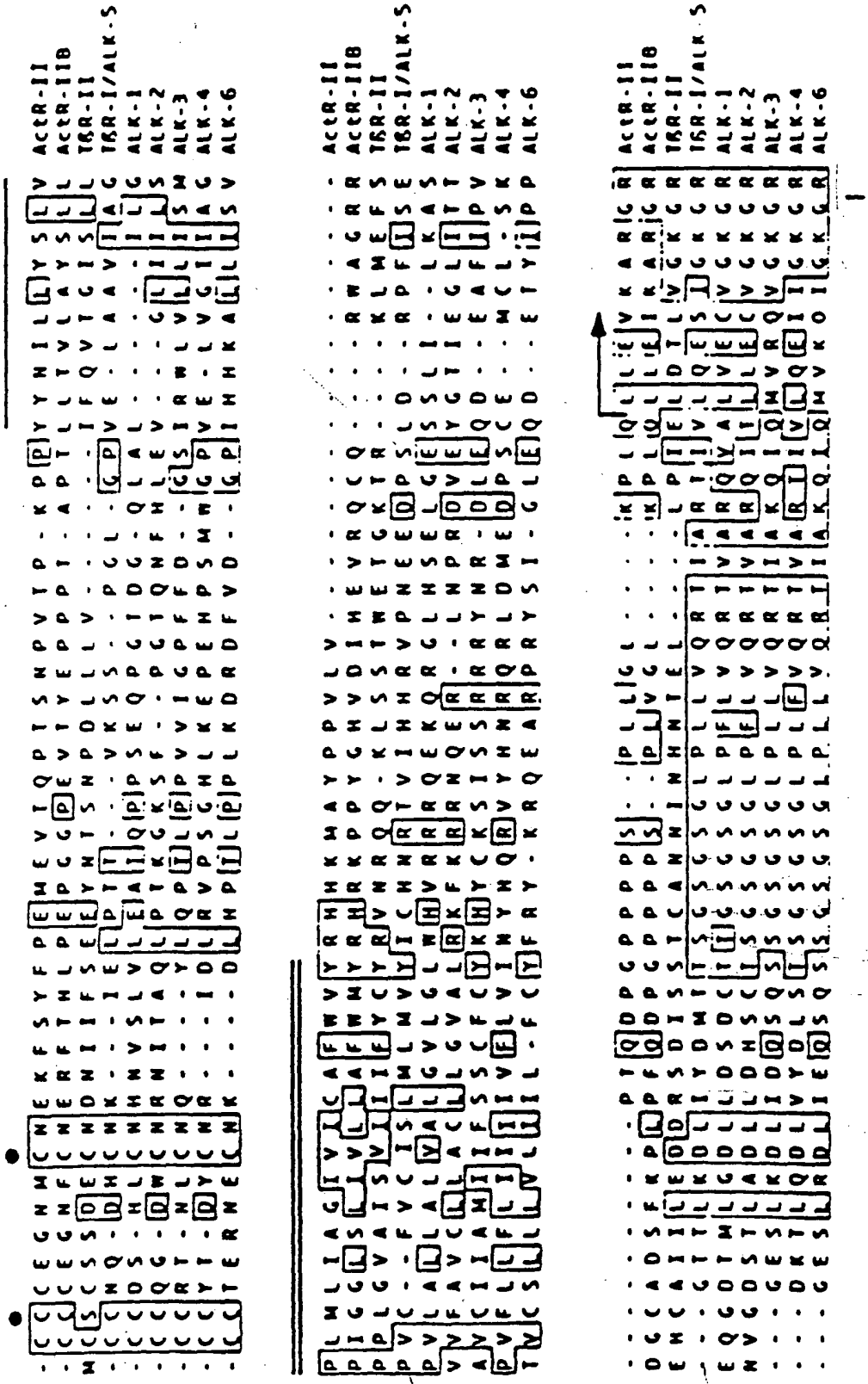

Fig. 3 contd.

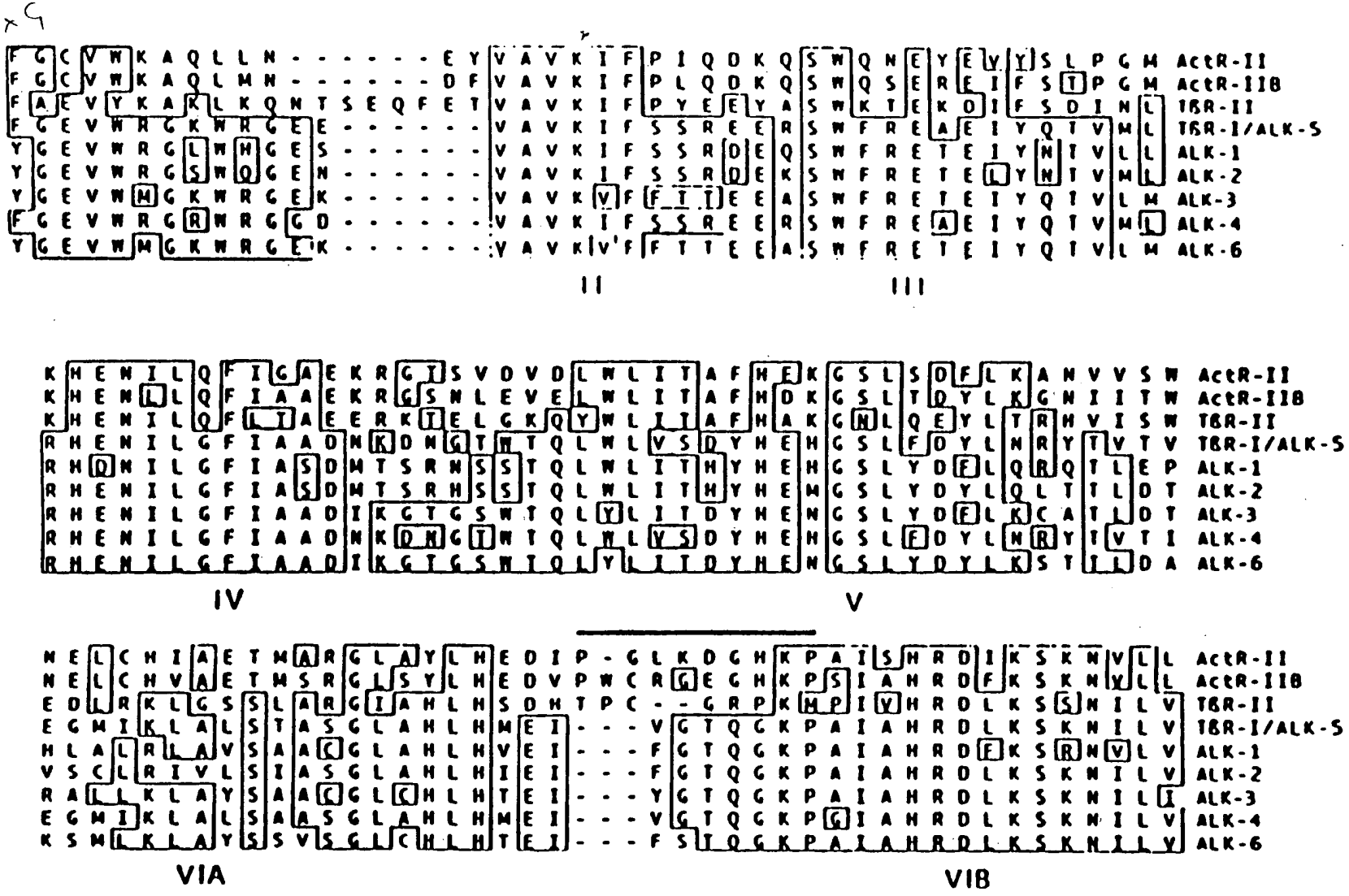

Fig. 3 contd.

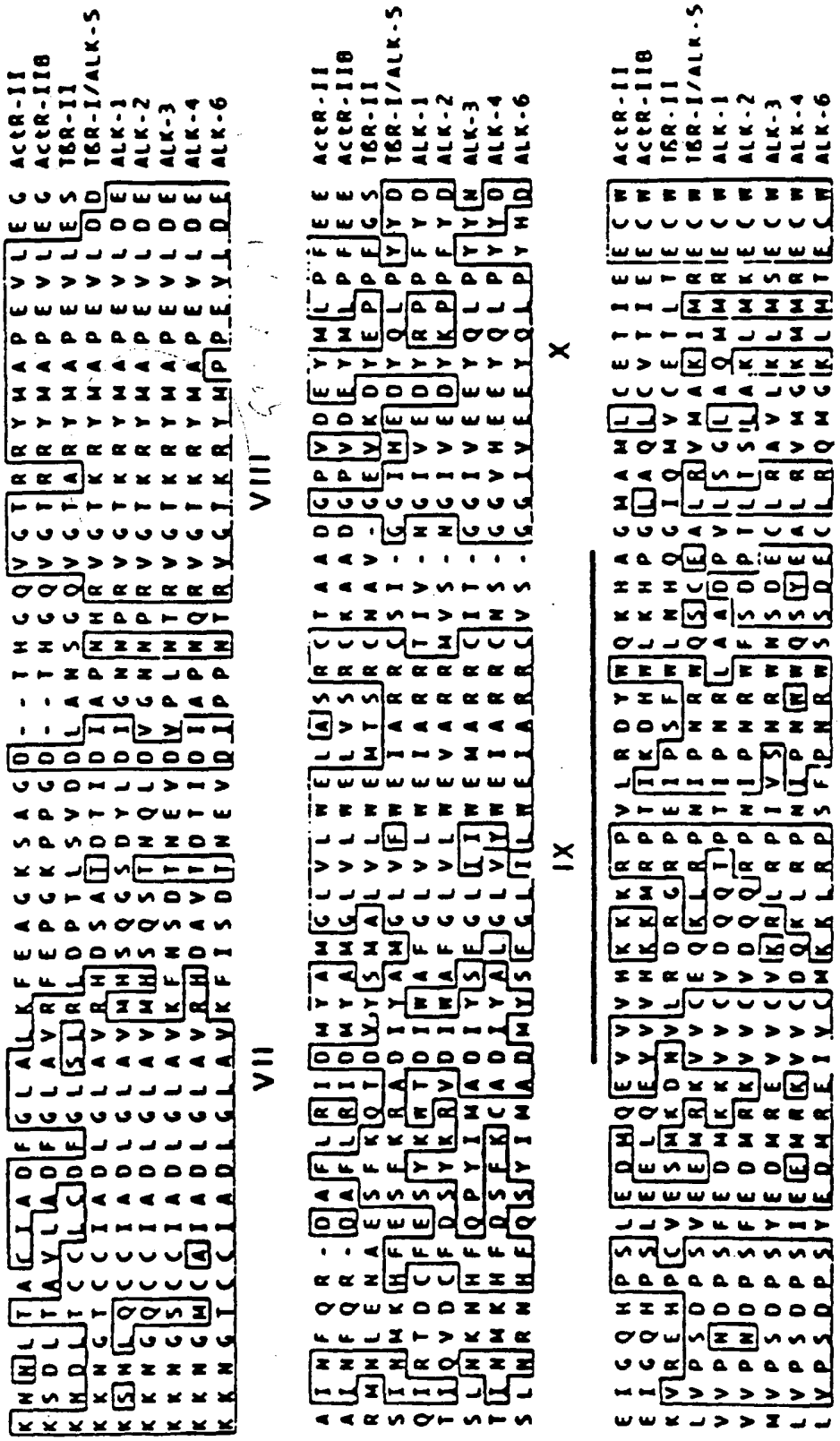
VII
VIII
IX
X
ActR-II
ActR-IIB
TBR-II
TBR-I/ALK-5
ALK-1
ALK-2
ALK-3
ALK-4
ALK-6

Fig. 3 contd.

ActR-II
ActR-IIB
TBR-II
TBR-I/ALK-5
ALK-1
ALK-2
ALK-3
ALK-4
ALK-6
(503)
(509)
(532)
(505)
(502)
XI
PKESSL (513) ActR-II
PKESSI (536) ActR-IIB
K (567) TBR-II

Fig. 3 contd.

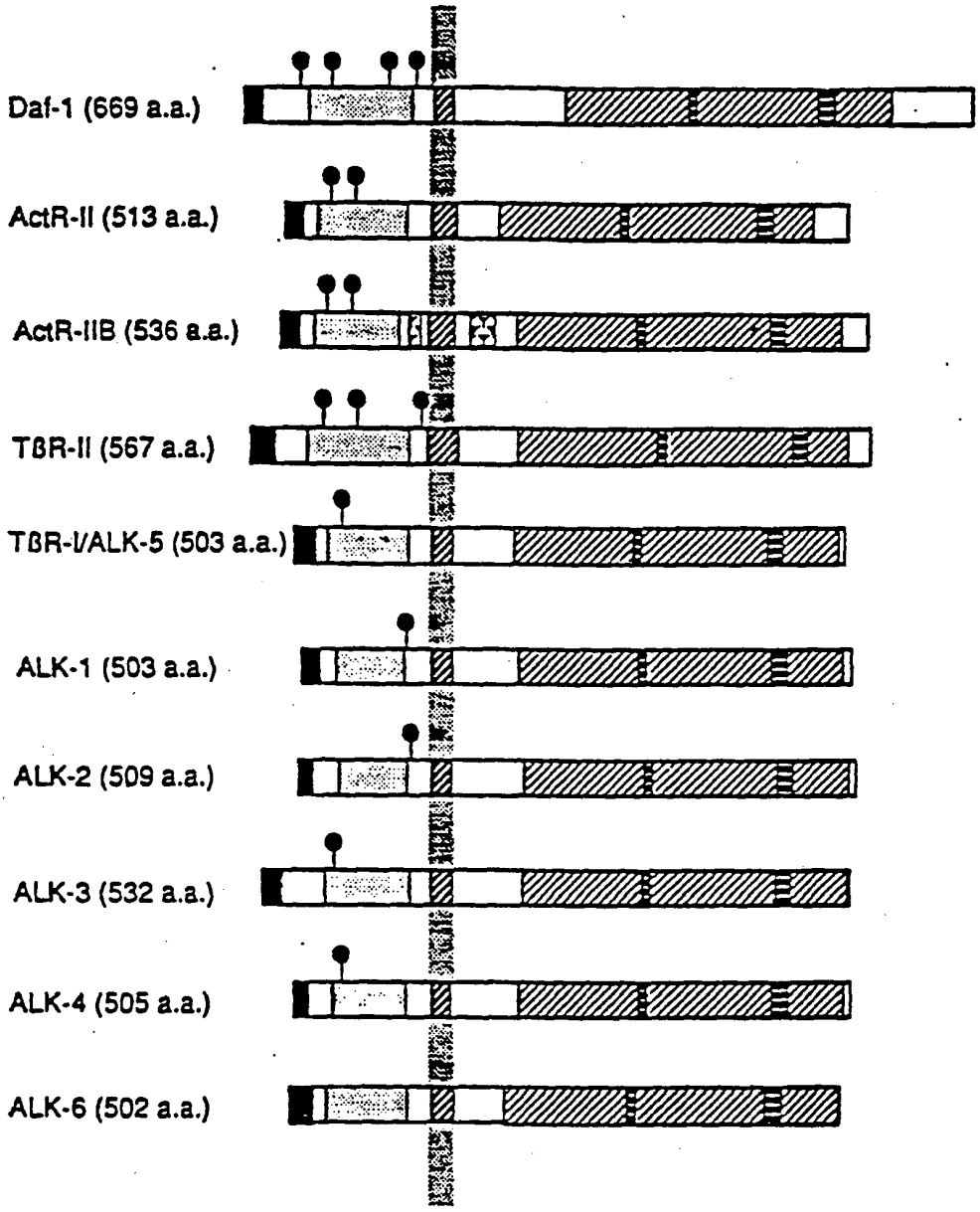
Daf-1 (669 a.a.)
ActR-II (513 a.a.)
ActR-IIB (536 a.a.)
TβR-II (567 a.a.)
TβR-I/ALK-5 (503 a.a.)
ALK-1 (503 a.a.)
ALK-2 (509 a.a.)
ALK-3 (532 a.a.)
ALK-4 (505 a.a.)
ALK-6 (502 a.a.)
signal sequence
cysteine-rich region
transmembrane domain
serine/threonine kinase domain
insert in the kinase domain
potential N-glycosylation site
alternatively spliced region

Fig. 4

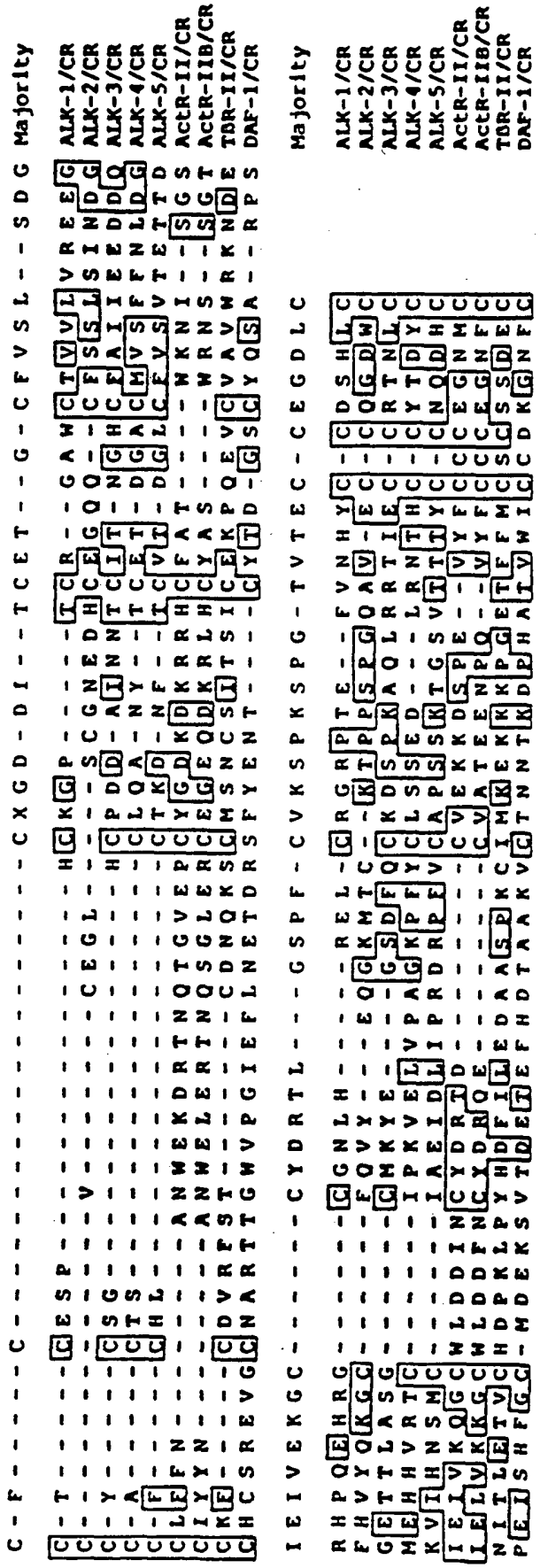
ALK-1/CR
ALK-2/CR
ALK-3/CR
ALK-4/CR
ALK-5/CR
ActR-II/CR
ActR-IIB/CR
TBR-II/CR
DAF-1/CR
Majority

Fig. 5

	ALK-2	ALK-3	ALK-4	ALK-5	ActR-II	ActR-IIB	TßR-II	daf-1	
ALK-1	79	60	61	63	40	40	37	39	
ALK-2		63	64	65	41	39	37	39	
ALK-3			63	65	41	38	37	39	
ALK-4				90	41	40	39	42	
ALK-5					42	40	41	43	
ActR-II						78	48	35	
ActR-IIB							47	32	
TßR-II								34	

Fig. 6

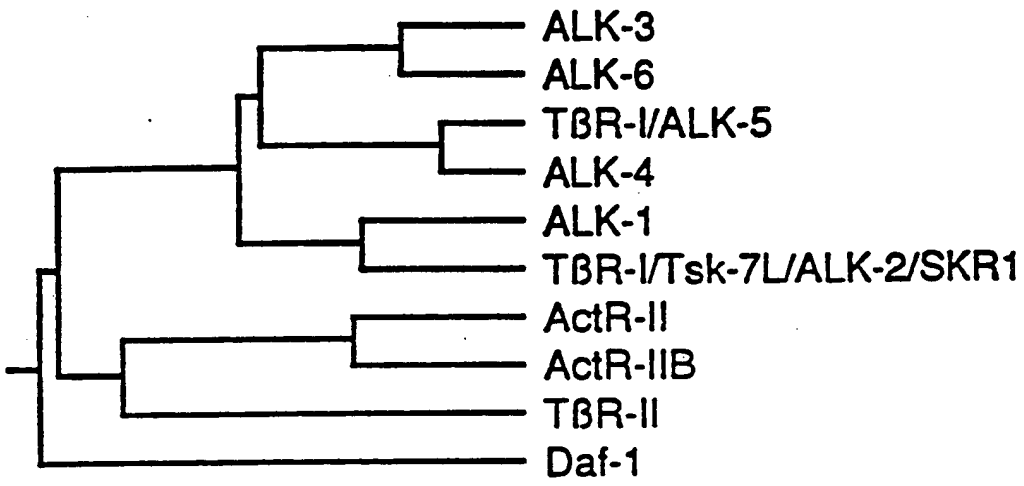
ALK-3
ALK-6
TβR-I/ALK-5
ALK-4
ALK-1
TβR-I/Tsk-7L/ALK-2/SKR1
ActR-II
ActR-IIB
TβR-II
Daf-1

Fig. 7